

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

10/5/8,868

Source:

PC+

Date Processed by STIC:

1-10-05

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/518,868

DATE: 01/10/2005

TIME: 15:32:51

Input Set : A:\Xenon 140.txt

Output Set: N:\CRF4\01102005\J518868.raw

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4 <110> APPLICANT: Xenon Genetics, Inc.
5   Warner-Lambert Company, LLC
7 <120> TITLE OF INVENTION: Novel Therapeutic Target for Treating Vascular Diseases,
8   Dyslipidemias and Related Disorders
10 <130> FILE REFERENCE: 760050-100
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/518,868
C--> 13 <141> CURRENT FILING DATE: 2004-12-17
15 <150> PRIOR APPLICATION NUMBER: US/60/391,878
16 <151> PRIOR FILING DATE: 2002-06-27
18 <160> NUMBER OF SEQ ID NOS: 32
20 <170> SOFTWARE: PatentIn Version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 501
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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29 cacacactgt gtgcctttat gtcctagaaa gatcttttga tatacaggac ctaaatggaa      120
30 tacattccac cccaaaataa acatgggtca tacatgcata ttatttcaat acacatatgt      180
31 caggaccatc ttcataaata ttcataagctc ctctataat ctgttaaata tgtgtgtgtg      240
32 tgcgtgtgtg tgtgtgtgtg tgtgtgtgtg tatagtttgt ttgttttgag agggagtctt      300
33 gctctgttgc ccaggctgga gtgcagcagt gcaatctcaa ctactataa cttccacctc      360
34 caggttcaag caattctcat gtctcagccg agtagctggg accacagtca catgccacca      420
35 ctcttggtta attttttttt tttttttttg agacggagtc tcgctctgtc acccaggcta      480
36 gagtgcagtg gcgcgatctt g                                     501
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 600
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
44 <400> SEQUENCE: 2
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46 tacagtgtgt ccttggttaa aggcagcctg ggcacactgc agtgccctgg tgtaacggac      120
47 agccatgggc cttgcacttg aactaggggc tggccccagg actgtgacat gtcaccctg      180
48 agccccgggt tctcctctga gaaatgctgg ggtcacctgc tttgagggct gttcttagta      240
49 tgaagcaaga gcacagtaag acaaaagact acagagccga cacacacaca cacacacaca      300
50 cacacacaca cacacacaca cagagtagtg cattccagaa caatatactc atttcatttt      360
51 cctgttgtca ttcagagagg cgagtgcact gggagccaca aaagtgcaat gttgcaaaga      420
52 cttttccaaa acaggatgcg taatggctgc tgtggccact gctggcggtg tgtggggata      480
53 cctgggtagc agcaggccac cagagagtgt gcatccctcc ttctgtgctc tgcagtgggg      540
54 ctcatTTTTT tgggcccagg tcttgccctgc ctgcaatcct cctctgatga cggagttacc      600
57 <210> SEQ ID NO: 3
58 <211> LENGTH: 4333
59 <212> TYPE: DNA

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60 <213> ORGANISM: Homo sapiens

62 <400> SEQUENCE: 3

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| 63 | atgtccttcc | ggggccacgc | agaaagtgcc | gccgctttgg | ccactcagag | cccccgggcc | 60 |
| 64 | gcggtcgtcg | tacgectgaa | ggcgggtcgt | gccggcggcc | gctctagtct | ccgcctccgc | 120 |
| 65 | tcaggccggt | cctccggggc | ttctcaatgg | tttcccggtg | gcctctcaat | ggttttcccg | 180 |
| 66 | gcggcccttg | cgccgacgcc | aggagacttc | cggagcttgg | tgacgtcacg | agcgagcttt | 240 |
| 67 | tctacccaaa | tacgcggcgg | gggaataggc | tcgagggcgg | tgagcagtga | caattgctag | 300 |
| 68 | gcggagacgt | tcgaggggag | agagacctta | gaaaggatca | ggactggcgg | gaggtattta | 360 |
| 69 | actgaaagga | atatctgctt | cactgttgca | accaaaccag | atgccttctt | ccacttcacc | 420 |
| 70 | agaccaagga | gatgacctgg | agaactgcat | tttaagattt | tctgacctgg | atttaaaaga | 480 |
| 71 | tatgagtctt | attaatccca | gcagcagtct | taaagcagaa | ttagatggca | gtacaaaaaa | 540 |
| 72 | gaaatactcg | tttgcaaaga | aaaaggcctt | tgcccttttt | gtcaaaacca | aagaagttcc | 600 |
| 73 | aacaaaaagg | agttttgaat | gtaaagaaaa | attgtggaaa | tgctgtcggc | agctattcac | 660 |
| 74 | agaccaaacc | agcatccata | gacatgtggc | aacacaacat | gctgatgaaa | tttatcacca | 720 |
| 75 | gacagcttct | attttaaagc | aactggctgt | gacattgagc | acctcaaaga | gtctttcgtc | 780 |
| 76 | tgcagatgaa | aagaaccctt | taaaagagtg | ccttccacat | agccatgacg | tgtctgcttg | 840 |
| 77 | gctccctgat | ataagctgct | ttaaccctga | tgagctgata | agtggccagg | gcagtgaaga | 900 |
| 78 | aggggaggtg | ctcctttatt | actgctacca | tgacctggag | gatccccaat | ggatctgtgc | 960 |
| 79 | ctggcagaca | gctctgtgtc | agcacctgca | cctcacaggc | aagattcgaa | ttgctgcaga | 1020 |
| 80 | aggaatcaat | gggacagttg | gtggaagcaa | attggctacc | agactttatg | tggaagtcat | 1080 |
| 81 | gctttccttc | ccattgttta | aggatgacct | gtgtaaagat | gattttaaga | ccagcaaagg | 1140 |
| 82 | aggagctcac | tgttttccag | aattgctgtg | tggtgtattt | gaagaaatcg | tgccccagg | 1200 |
| 83 | gatcagcccc | aaaaagatct | cctacaagaa | gcttgaatc | catttatccc | caggtgaatt | 1260 |
| 84 | tcataaagaa | gtagaaaagt | ttttatctca | ggcaaataca | gaacaaagtg | atactatcct | 1320 |
| 85 | tcttgattgc | agaaacttct | atgaaagcaa | aataggacga | ttccaaggct | gcttagcccc | 1380 |
| 86 | agacatcagg | aaattcagtt | acttccctag | ctacgttgac | aaaaatctag | aacttttcag | 1440 |
| 87 | agagaagaga | gtgctgatgt | actgtaccgg | gggcatccgc | tgtgagcggg | gttcagccta | 1500 |
| 88 | cctcaaagcc | aaggagtggt | gcaaggaggt | gttccagctc | aagggtggca | tccacaagta | 1560 |
| 89 | cctggaagag | tttctgatg | gcttttacaa | aggggaagtg | tttgtttttg | atgaacgcta | 1620 |
| 90 | tgtctgttcc | tacaacagtg | atgtggtgtc | agagtgttca | tactgtggag | cccgtgggga | 1680 |
| 91 | ccagtataaa | ctctgtctca | ctccccagtg | ccgccagctc | gttttgacct | gccctgcctg | 1740 |
| 92 | tcaaggacaa | ggattcacag | cctgttggtg | cacatgtcaa | gacaagggga | gcaggaaagt | 1800 |
| 93 | ttcaggccct | atgcaagaca | gctttaaaga | ggaatgcgag | tgacacagcc | gacggccacg | 1860 |
| 94 | catacctagg | gaactcttgc | agcatgtgcg | acagcctgtg | agcccagagc | cagggcctga | 1920 |
| 95 | tgtctgatgag | gatgggcccag | tgtttatgtg | agcagcacct | ttggcatttt | cccaggccct | 1980 |
| 96 | cggtaaaagt | aggtttgggg | tgactataca | gagaaagcat | ggcaagactg | cagaaacaga | 2040 |
| 97 | gaaatcggga | acttcagttc | tggecgctgc | caccgtggca | gccgtctaca | cttcacagcg | 2100 |
| 98 | ggaggggagg | agtcacgttg | tctaccactt | acctgagaca | ttctgatttg | gatgatgcta | 2160 |
| 99 | gagcacagaa | aataggtgag | ctgcatggga | tcccaaagct | gctgagggat | agagcctgag | 2220 |
| 100 | cctggtggcc | acagcatatg | ccctttctgt | tccatgcagc | tggggctggt | agtagtcatt | 2280 |
| 101 | gcccttgtca | gcagaccttc | taccctgggtg | gcaaacacat | gaaagctgtg | gccctgggag | 2340 |
| 102 | tggcctccta | aaacaagcca | cttaggtcat | ctgccateta | cccttaacct | ctgtctctcg | 2400 |
| 103 | cctgagggga | atctgcaagc | tgtgcattgg | gcttacctcc | tgtttttgta | gaaataacca | 2460 |
| 104 | tcctttggta | tacatggagg | atagttccag | aacgcctgag | tatacaaaaa | cccaatgcat | 2520 |
| 105 | actcaagtc | cacagtgggc | cctacagaac | ccacgtatgt | gataaatcag | ccctccatgt | 2580 |
| 106 | acgcaggttt | cgccccctgc | caatactgta | ttttcaacct | gtatgggtga | aaaaaatcca | 2640 |
| 107 | tatataagtg | cagccatgca | gttcaaacc | atattgttca | agggccaact | gtatagttta | 2700 |
| 108 | ttgaacagcc | acacccattc | ctttacacat | gatctatggc | agagttgaat | agttgcaaca | 2760 |
| 109 | gacactatgt | ggcctgcaaa | atcggaat | tttactgtct | ggccttttac | agaaaagt | 2820 |

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110 gccagccct gatctagacc agcagctcat ctgatagagg cagaggtggc cttaaagatg 2880
111 tggccttctt cattttctgt tggtttggtt tcgtttctat gagagatttc ctctgatagc 2940
112 tctgctttcc ccagcactta ctctctgagc ttttaaagt tctctctggg agcttcatat 3000
113 aagctcgggtg acatttgagc cacagttttt agatcagcac ctggaataca tgacacattc 3060
114 ttactgaggt catccagcac tgccatgggt gctgcccagt cttctggcca gtgtgccagg 3120
115 cacatgtccc tgtcacacag gttccaagaa acacatacgc agccatgcat agaccaacag 3180
116 atttaatat atattgcagt tttcagcgat gcagaatgca gctgcaattg tgttttaagg 3240
117 agaagccaaa tggggatggt tgtccctgca acatggtgcc actcctgggc catgtgcagc 3300
118 ctgagtggac actcttccat agcgctgagg ccctggcccc gcctccagtt accctgtact 3360
119 gccactgcc ttacagttca gtgcgcaggc cttcaccttt tcatcaccag cctctctgct 3420
120 cagtgtctctg gagttcttga cctgttcctt tatcatgaga tttgctgaaa tcactaatga 3480
121 aaataactcc caaagcaac aaacaaaaat attagtttaa ctggcactgt ggtatattaa 3540
122 aaggcacaag ggcattgtgg cttaacactt ttgctggatc ccaagagacg cacatgatgt 3600
123 taaaaagaga tctggcagca gtactaatac tacatttcag tgtaatcatc ttgggggtgg 3660
124 ttggccagga tttcccaatt ccttgatatac tggagtttct tcaccattgt ccggcatcct 3720
125 gcggaggctt aatatacagg cgtaagggtca gcagcaattt gtctaataag tgatgagatc 3780
126 agtagctgaa gtctctaagc tggggccatta ctaaaacca tagccatggt gatctggaaa 3840
127 tttatccctc tagtgtctta cctcacataa gccatttgcc cactgtgcaa tatagaaagg 3900
128 tgttttcaaa agtatttggc cgtagatttt cacatccatc ataaggtttg cattcaataa 3960
129 ggaaaaagtt ctaactccag tattaatttg tacataaatc ccaaagtgc ttaaagaaca 4020
130 ctgagggaca tgtttggtgc ctgggattgg taatgaaagg ttggtttttg aaacttgaaa 4080
131 tttcaccatt ggtttttttc ctatcatttc tgcataatcca gcaaaaggaa tctcatgttg 4140
132 actcctggca gagttcagtg gcttcagttc gtctatctgt tctgagggga aaattgtgtt 4200
133 ctggatccag taatcaattt ggcaacttta atcgaggttt tcaaaattcc aaggagggtt 4260
134 aataaagaat gataatcagt tttatttgc t aatagctaag acaaatttgt aataaagtgt 4320
135 tttataatac ttc 4333
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 516
140 <212> TYPE: PRT
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 4
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145 1 5 10 15
147 Ile Leu Arg Phe Ser Asp Leu Asp Leu Lys Asp Met Ser Leu Ile Asn
148 20 25 30
150 Pro Ser Ser Ser Leu Lys Ala Glu Leu Asp Gly Ser Thr Lys Lys Lys
151 35 40 45
153 Tyr Ser Phe Ala Lys Lys Lys Ala Phe Ala Leu Phe Val Lys Thr Lys
154 50 55 60
156 Glu Val Pro Thr Lys Arg Ser Phe Glu Cys Lys Glu Lys Leu Trp Lys
157 65 70 75 80
159 Cys Cys Arg Gln Leu Phe Thr Asp Gln Thr Ser Ile His Arg His Val
160 85 90 95
162 Ala Thr Gln His Ala Asp Glu Ile Tyr His Gln Thr Ala Ser Ile Leu
163 100 105 110
165 Lys Gln Leu Ala Val Thr Leu Ser Thr Ser Lys Ser Leu Ser Ser Ala
166 115 120 125
168 Asp Glu Lys Asn Pro Leu Lys Glu Cys Leu Pro His Ser His Asp Val
169 130 135 140

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171 Ser Ala Trp Leu Pro Asp Ile Ser Cys Phe Asn Pro Asp Glu Leu Ile
172 145 150 155 160
174 Ser Gly Gln Gly Ser Glu Glu Gly Glu Val Leu Leu Tyr Tyr Cys Tyr
175 165 170 175
177 His Asp Leu Glu Asp Pro Gln Trp Ile Cys Ala Trp Gln Thr Ala Leu
178 180 185 190
180 Cys Gln His Leu His Leu Thr Gly Lys Ile Arg Ile Ala Ala Glu Gly
181 195 200 205
183 Ile Asn Gly Thr Val Gly Gly Ser Lys Leu Ala Thr Arg Leu Tyr Val
184 210 215 220
186 Glu Val Met Leu Ser Phe Pro Leu Phe Lys Asp Asp Leu Cys Lys Asp
187 225 230 235 240
189 Asp Phe Lys Thr Ser Lys Gly Gly Ala His Cys Phe Pro Glu Leu Arg
190 245 250 255
192 Val Gly Val Phe Glu Glu Ile Val Pro Met Gly Ile Ser Pro Lys Lys
193 260 265 270
195 Ile Ser Tyr Lys Lys Pro Gly Ile His Leu Ser Pro Gly Glu Phe His
196 275 280 285
198 Lys Glu Val Glu Lys Phe Leu Ser Gln Ala Asn Gln Glu Gln Ser Asp
199 290 295 300
201 Thr Ile Leu Leu Asp Cys Arg Asn Phe Tyr Glu Ser Lys Ile Gly Arg
202 305 310 315 320
204 Phe Gln Gly Cys Leu Ala Pro Asp Ile Arg Lys Phe Ser Tyr Phe Pro
205 325 330 335
207 Ser Tyr Val Asp Lys Asn Leu Glu Leu Phe Arg Glu Lys Arg Val Leu
208 340 345 350
210 Met Tyr Cys Thr Gly Gly Ile Arg Cys Glu Arg Gly Ser Ala Tyr Leu
211 355 360 365
213 Lys Ala Lys Gly Val Cys Lys Glu Val Phe Gln Leu Lys Gly Gly Ile
214 370 375 380
216 His Lys Tyr Leu Glu Glu Phe Pro Asp Gly Phe Tyr Lys Gly Lys Leu
217 385 390 395 400
219 Phe Val Phe Asp Glu Arg Tyr Ala Leu Ser Tyr Asn Ser Asp Val Val
220 405 410 415
222 Ser Glu Cys Ser Tyr Cys Gly Ala Arg Trp Asp Gln Tyr Lys Leu Cys
223 420 425 430
225 Ser Thr Pro Gln Cys Arg Gln Leu Val Leu Thr Cys Pro Ala Cys Gln
226 435 440 445
228 Gly Gln Gly Phe Thr Ala Cys Cys Val Thr Cys Gln Asp Lys Gly Ser
229 450 455 460
231 Arg Lys Val Ser Gly Pro Met Gln Asp Ser Phe Lys Glu Glu Cys Glu
232 465 470 475 480
234 Cys Thr Ala Arg Arg Pro Arg Ile Pro Arg Glu Leu Leu Gln His Val
235 485 490 495
237 Arg Gln Pro Val Ser Pro Glu Pro Gly Pro Asp Ala Asp Glu Asp Gly
238 500 505 510
240 Pro Val Leu Met
241 515
244 <210> SEQ ID NO: 5

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245 <211> LENGTH: 526
246 <212> TYPE: PRT
247 <213> ORGANISM: Mus musculus
249 <400> SEQUENCE: 5
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251 1 5 10 15
253 Val Leu Lys Val Phe Asp Leu Asp Leu Lys Glu Ser Asn Leu Val Asn
254 20 25 30
256 Pro Ser Asn Ser Leu Lys Ala Glu Leu Asp Gly Ser Thr Lys Lys Lys
257 35 40 45
259 Tyr Ser Phe Ala Lys Lys Lys Ala Phe Ala Leu Leu Val Lys Thr Lys
260 50 55 60
262 Gln Val Pro Ala Pro Ser Tyr Glu Phe Lys Gly Lys Arg Trp Arg Cys
263 65 70 75 80
265 Cys Gln Gln Leu Phe Ala Asp Gln Ile Ser Ile His Arg His Val Ala
266 85 90 95
268 Thr Gln His Ala Glu Asp Val Tyr Gln Gln Thr Ala Ser Leu Leu Lys
269 100 105 110
271 Gln Leu Thr Ala Ala Leu Ser Ala Ser Gln Ser Leu Thr Pro Thr Asp
272 115 120 125
274 Lys Arg Ser Ser Pro Lys Asp Cys Leu Thr Pro Ser Gln Glu Val Ser
275 130 135 140
277 Ala Trp Leu Pro Asp Val Ser His Val Ser Pro Gln Glu Leu Arg Ser
278 145 150 155 160
280 Gly Gln Val Thr Glu Glu Arg Glu Val Leu Leu Tyr Tyr Cys Tyr Cys
281 165 170 175
283 Asp Leu Glu Asp Pro His Trp Val Cys Ala Trp Gln Thr Ala Leu Cys
284 180 185 190
286 His His Leu His Leu Thr Gly Lys Ile Arg Ile Ala Thr Glu Gly Ile
287 195 200 205
289 Asn Gly Thr Val Gly Gly Ser Lys Val Ala Thr Arg Leu Tyr Val Glu
290 210 215 220
292 Val Met Leu Ser Cys Pro Leu Phe Lys Asp Tyr Leu Ser Glu Asp Asp
293 225 230 235 240
295 Phe Lys Ser Ser Lys Gly Gly Ser His Cys Phe Pro Glu Leu Arg Val
296 245 250 255
298 Gly Val Phe Glu Glu Ile Val Pro Met Gly Ile Ser Pro Ser Gln Val
299 260 265 270
301 Ser Tyr Lys Lys Pro Gly Ile His Leu Ser Pro Gly Glu Phe His Lys
302 275 280 285
304 Glu Ile Glu Lys Leu Leu Ser Gln Ser Ser Glu Glu Gln Gly Asn Thr
305 290 295 300
307 Ile Ile Leu Asp Cys Arg Asn Phe Tyr Glu Ser Lys Ile Gly Arg Phe
308 305 310 315 320
310 Gln Gly Cys Leu Ala Pro Asp Ile Arg Lys Phe Ser Tyr Phe Pro Ser
311 325 330 335
313 Tyr Val Asp Lys Asn Leu Asp Ile Phe Arg Gln Lys Arg Val Leu Met
314 340 345 350
316 Tyr Cys Thr Gly Gly Ile Arg Cys Glu Arg Gly Ser Ala Tyr Leu Arg

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date